

FIG. 1A

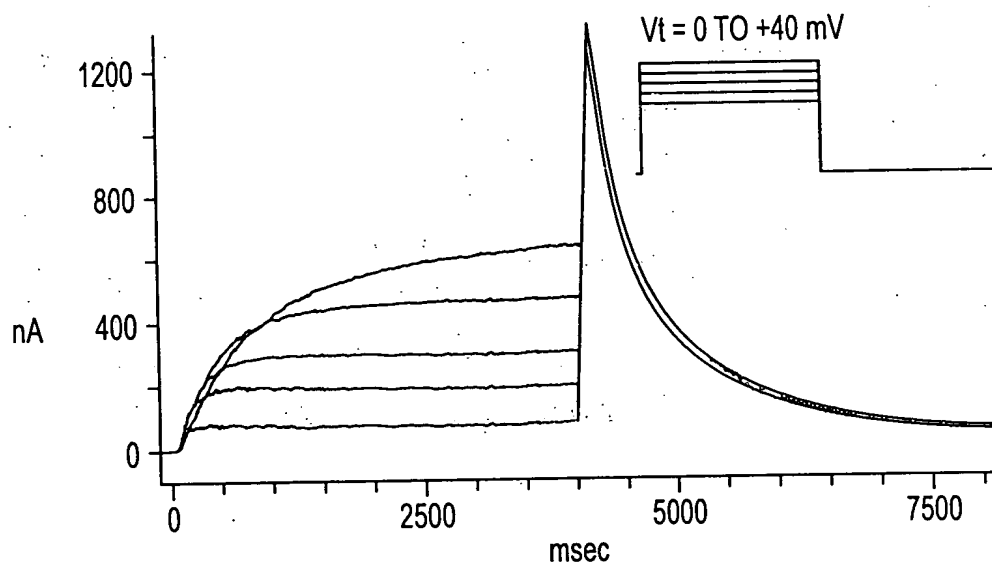
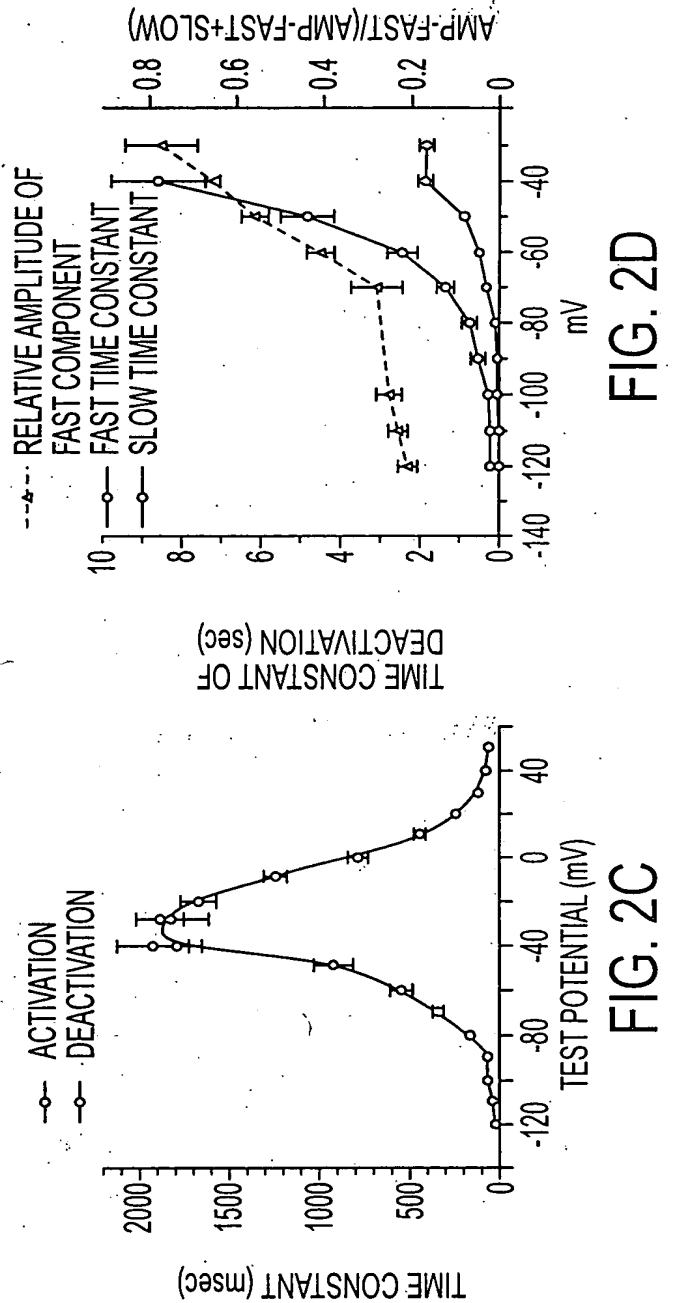
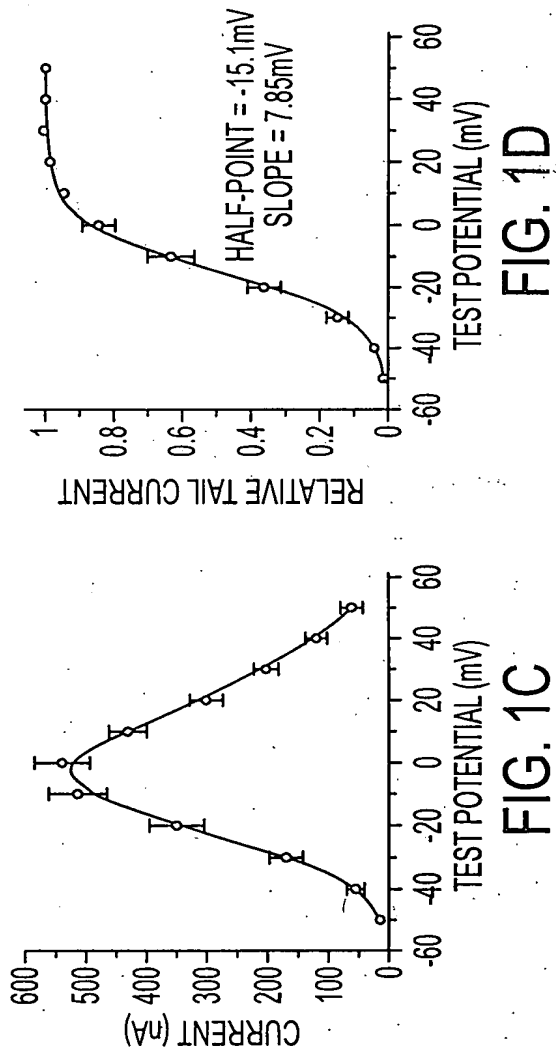


FIG. 1B



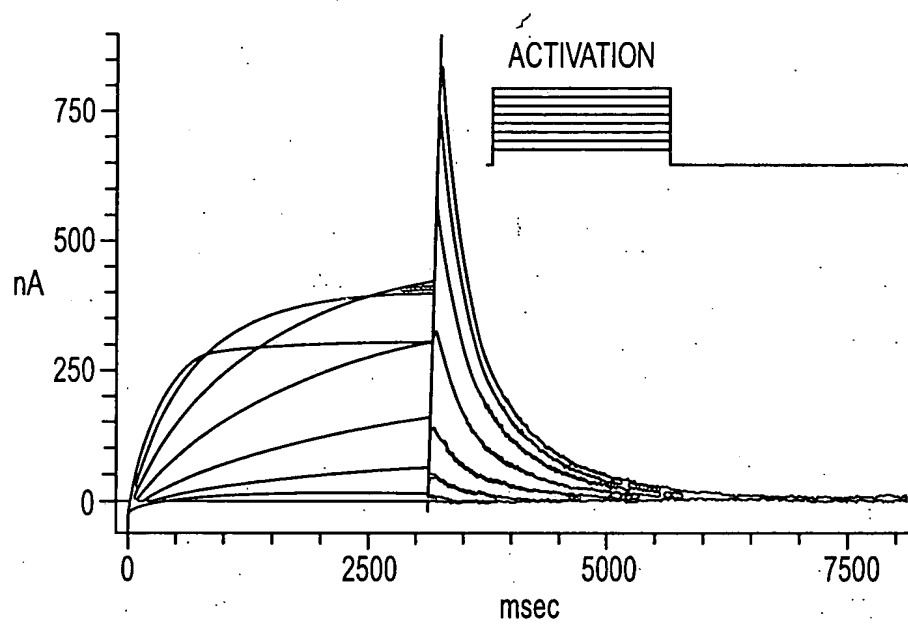


FIG. 2A

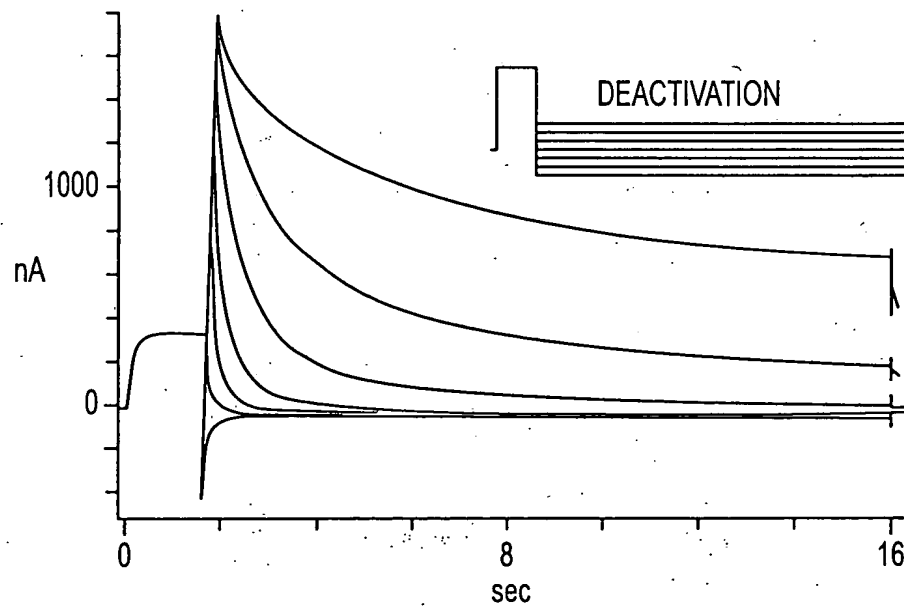


FIG. 2B

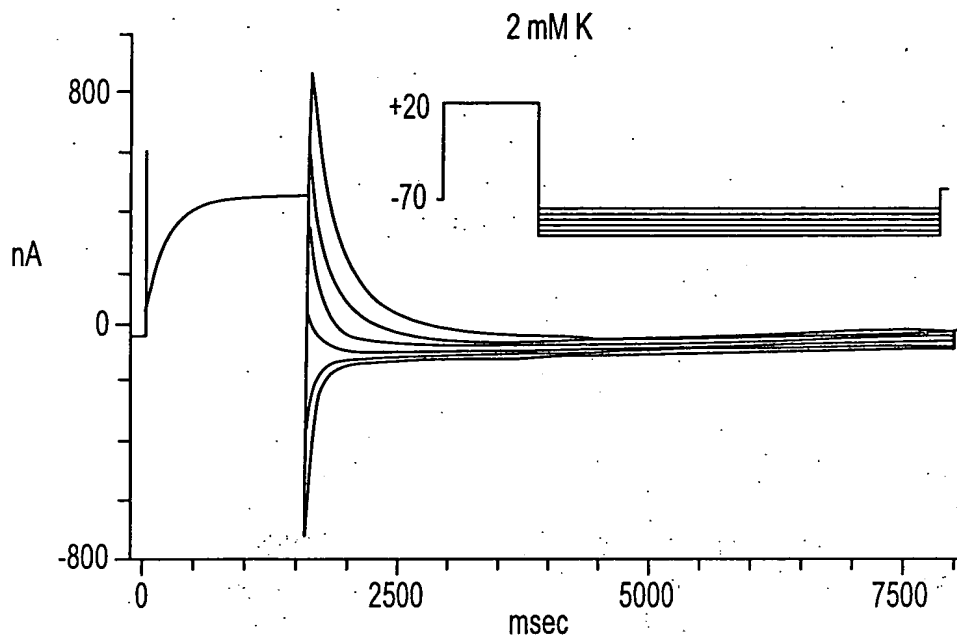


FIG. 3A

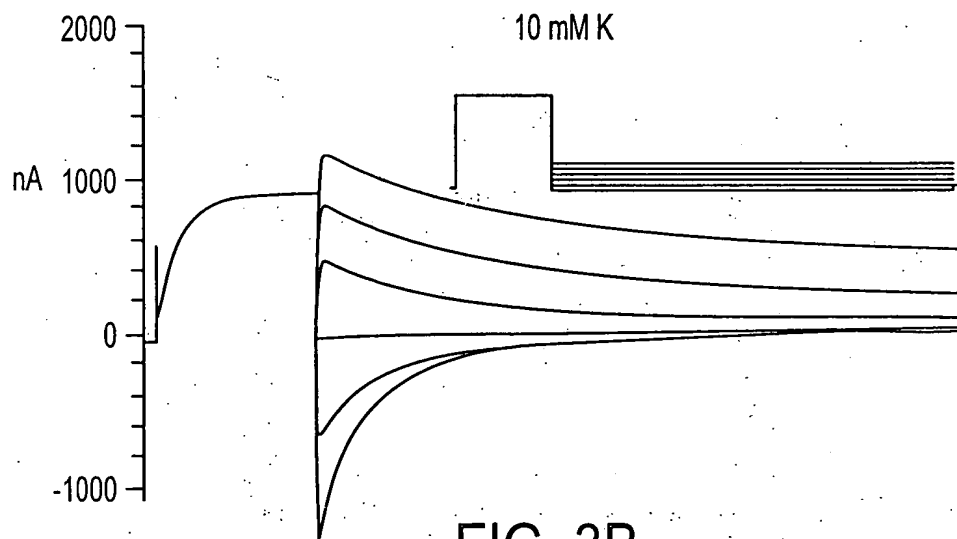


FIG. 3B

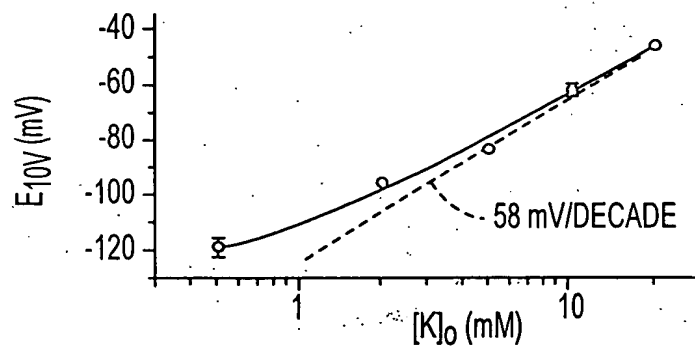


FIG. 3C

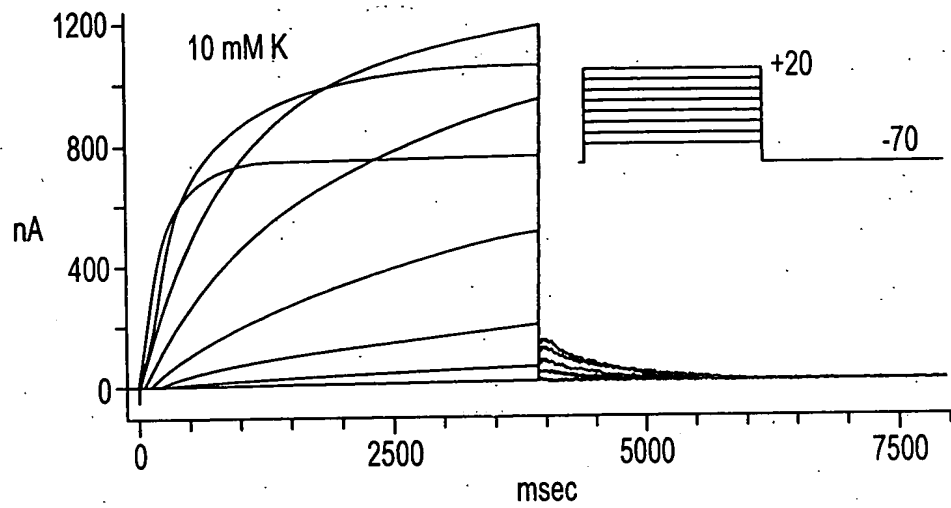


FIG. 4A

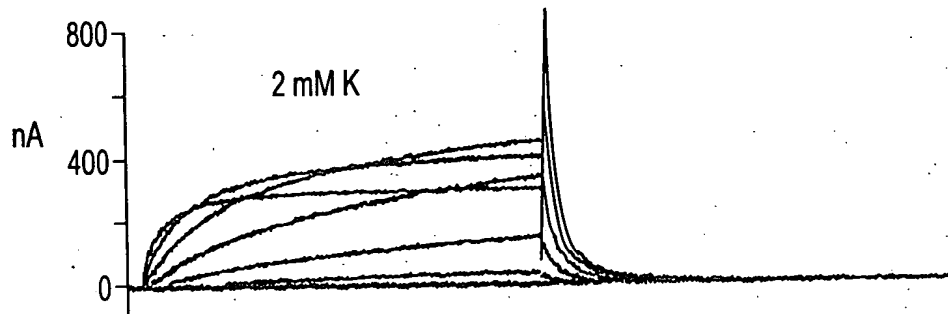


FIG. 4B

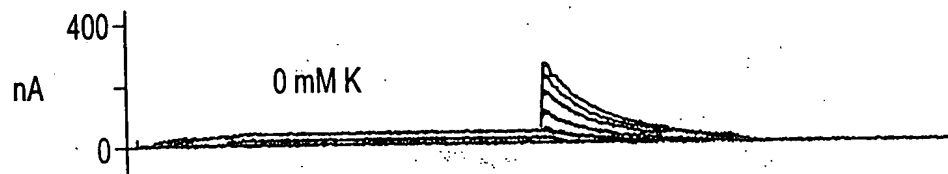


FIG. 4C

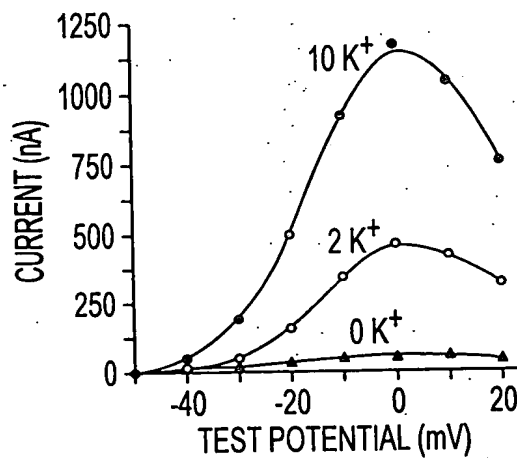


FIG. 4D

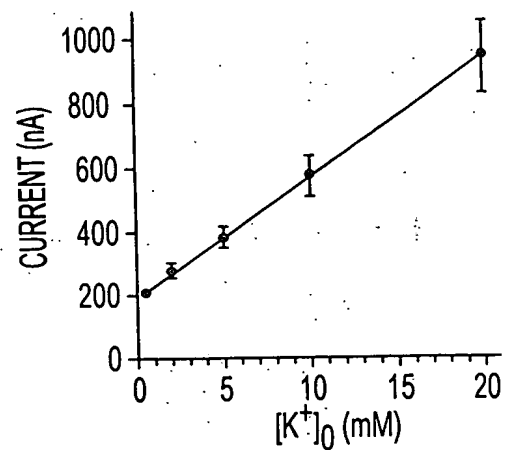


FIG. 4E

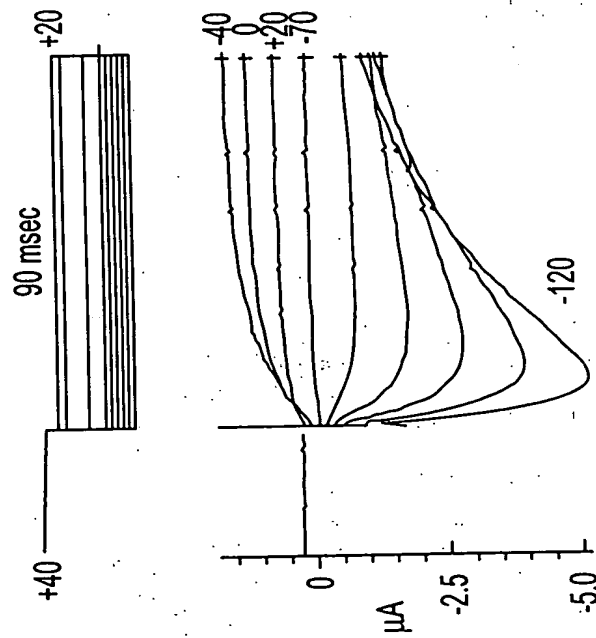


FIG. 5A

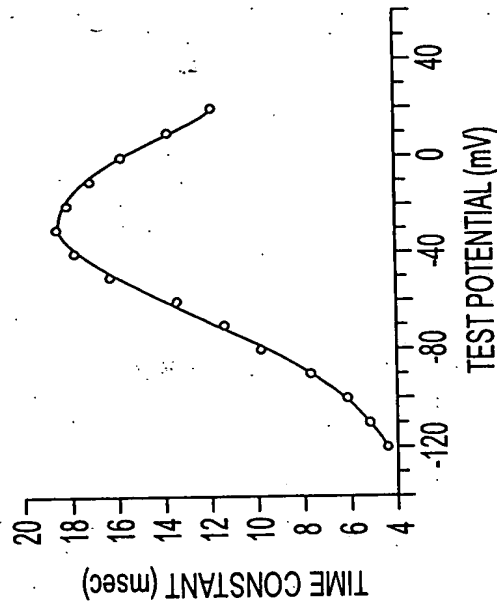


FIG. 5B

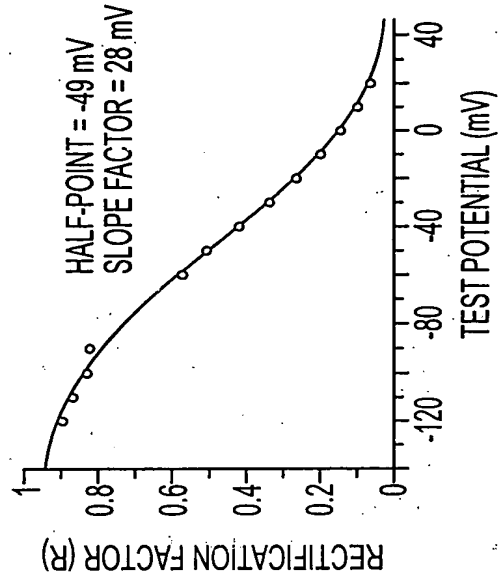


FIG. 5D

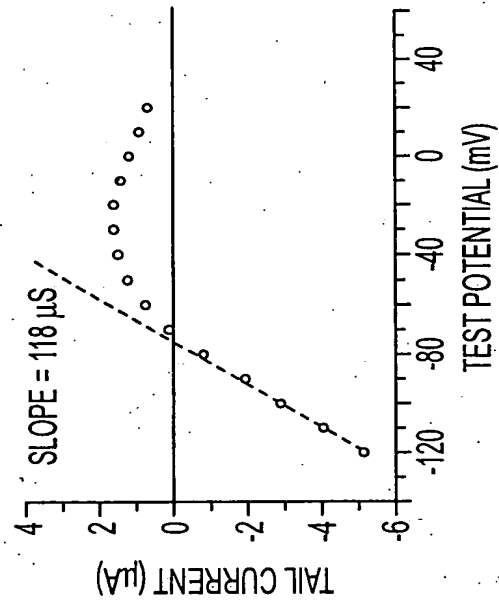


FIG. 5C

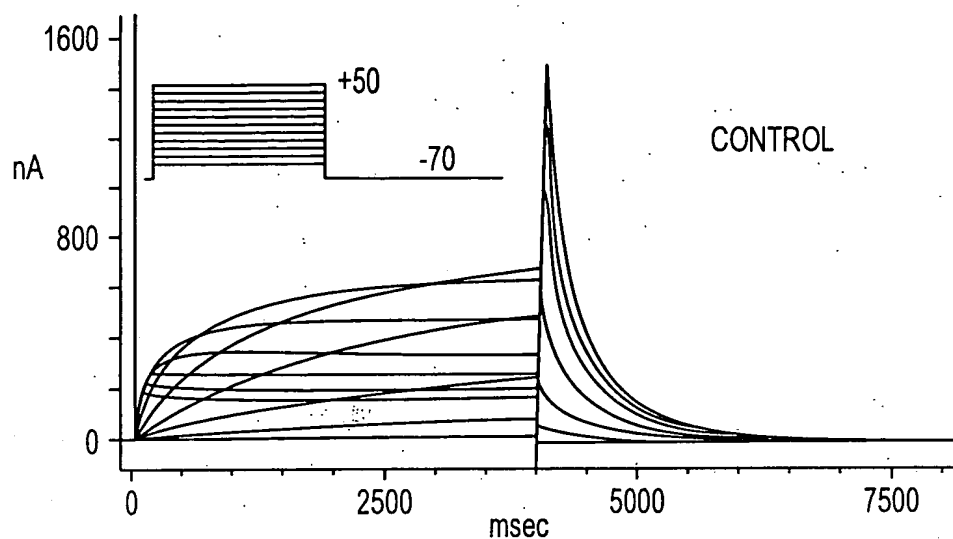


FIG. 6A

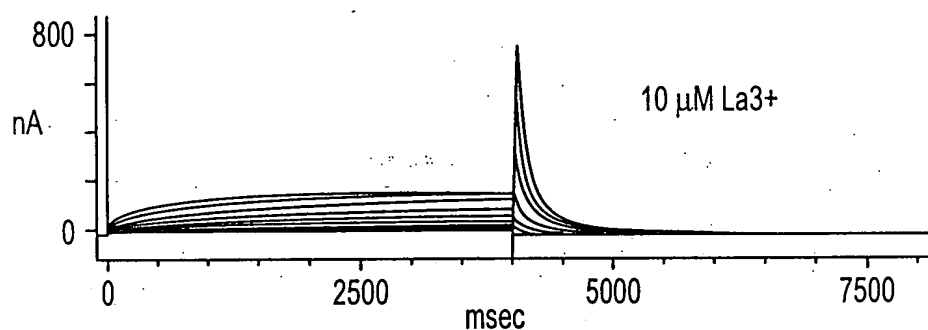


FIG. 6B

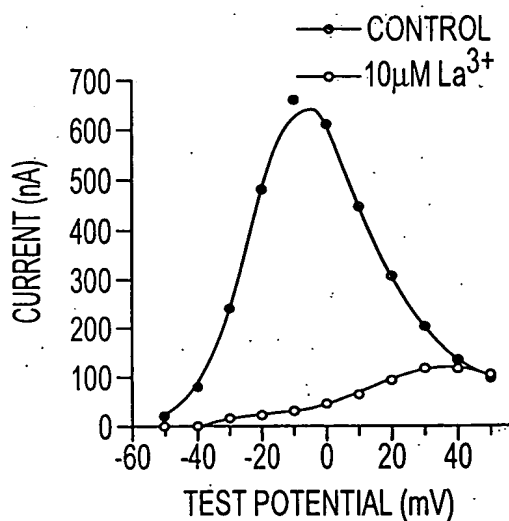


FIG. 6C

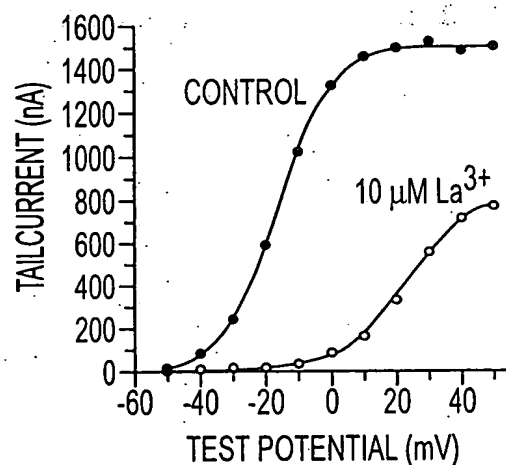


FIG. 6D

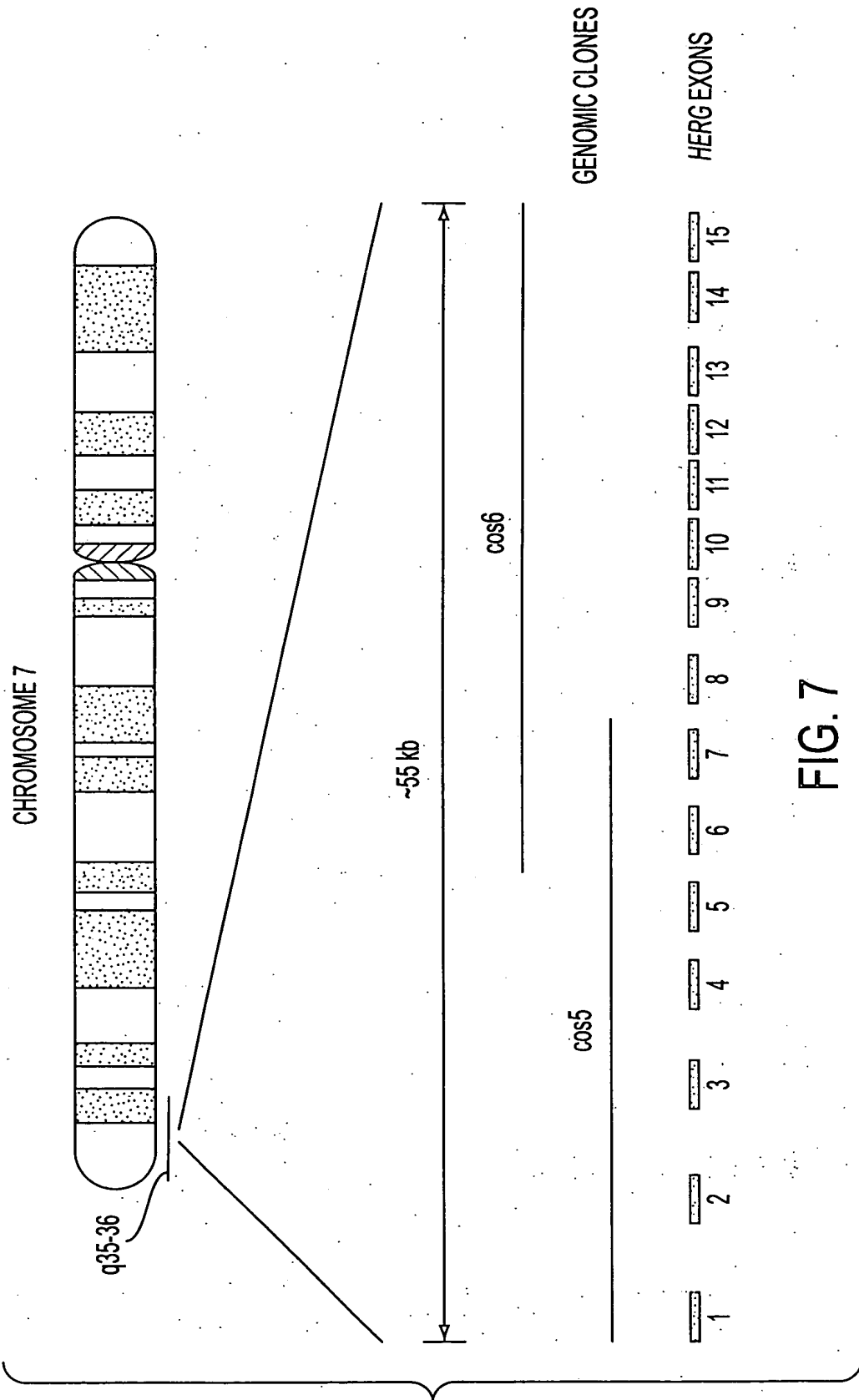


FIG. 7

AGCCTAGTGCTGGGCCGGGCCGGGGTGGGTGGGGCCCCGCCGCCCATGGGCTCAGGATGCCGGTGCGGAGG-81
 GGCCACGTCGCGCCGAGAACACCTTCTGGACACCATCATCCGCAAGTTTGAGGGCCAGAGCCGTAAGTTCATCATCGCC-162
 G H V A P Q N T F L D T I I R K F E G O S R K F I I A -32
 AACGCTCGGGTGGAGAACTGCGCCGTCATCTACTGCAACGACGGCTTCTGCGAGCTGTGCGGCTACTCGCGGGCCGAGGTG-243
 N A R V E N C A V I Y C N D G F C E L C G Y S R A E V -59
 ATGCAGCGACCTGCACCTGCGACTTCTGACGGGCCGCGCAGCAGCGCGCTGCCGCGCAGATCGCGCAGGCACTG-324
 M Q R P C T C D F L H G P R T Q R R A A A Q I A Q A L -86
 CTGGGCGCCGAGGAGCGCAAAGTGGAAATCGCCTTCTACCGAAAGATGGGAGCTGCTTCTATGTCTGGTGGATGTGGTG-405
 L G A E E R K V E I A F Y R K D G S C F L C L V D V V -113
 CCCGTGAAGAACGAGGATGGGGCTGTCATCATGTTTCATCTCAATTCGAGGTGGTGATGGAGAAGGACATGGTGGGGTCC-486
 P V K N E D G A V I M F I L N F E V V M E K D M V G S -140
 CCGGCTCATGACACCAACCACCGGGCCCCCCCCACCAGCTGGCTGGCCCCAGCGCGCCAAGACCTTCCGCCTGAAGCTG-567
 P A H D T N H R G P P T S W L A P G R A K T F R L K L -167
 CCCGCGTCTGGCGCTGACGGCCCCGGAGTCGTGGTGGCTGGGGCGCGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCG-648
 P A L L A L T A R E S S V R S G G A G A G A P G A V -194
 GTGGTGGACGTGACCTGACGCCCGCGGACCCAGCAGCTGCGCTGGCCCTGGACGAAGTGACAGCCATGGACAACCAC-729
 V V D V D L T P A A P S S E S L A L D E V T A M D N H -221
 GTGGCAGGGCTCGGGCCCCGGAGGAGCGCGTGGCTGGTGGGTCCCGGCTCTCCGCCCCGACGCGCGCCCCGGCCAGCTC-810
 V A G L G P A E E R R A L V G P G S P P R S A P G O L -248
 CCATCGCCCCGGGCGCACAGCCTCAACCCCGACGCTCGGGCTCCAGCTGCAGCTGGCCCCGACGCGCTCCCGAGAAAGC-891
 P S P R A H S L N P D A S G S S C S L A R T R S R E S -275
 TGCGCCAGCGTGCGCCGCGCTCGTGGCCGACGACATCGAGGCCATGCGCGCCGGGGTGTGCCCCCGCCACCGCGCCAC-972
 C A S V R R A S S A D D I E A M R A G V L P P P P R H -302
 GCCAGCACCGGGCCATGCACCCACTGCGCAGCGGCTTGCTCAACTCCACCTCGGACTCCGACCTCGTGGCTACCGCACC-1053
 A S T G A M H P L R S G L L N S T S D S D L V R Y R T -329
 ATTAGCAAGATTCCTCAAATCACCTCAACTTTGTGGACCTCAAGGGCGACCCCTTCTTGGCTTCGCCCCACAGTGACCGT-1134
 I S K I P Q I T L N F V D L K G D P F L A S P T S D R -356
 GAGATCATAGCACCTAAGATAAAGGAGCGAACCACAATGTCACTGAGAAGGTCACCCAGGTCCTGCTCCCTGGGCGCCGAC-1215
 E I I A P K I K E R T H N V T E K V T Q V L S L G A D -383
 GTGCTGCCTGAGTACAAGCTGCAGGCACCGCGCATCCACCGCTGGACCATCTGCATTACAGCCCTTCAAGGCCGTGTGG-1296
 V L P E Y K L Q A P R I H R W T I L H Y S P F K A V W -410
 GACTGGCTCATCTGCTGCTGGTCACTACACGGCTGTCTTACACCCTACTCGGCTGCCTTCTGCTGAAGGAGACGGAA-1377
 D W L I L L L V I Y T A V F T P Y S A A F L L K E T E -437
 GAAGGCCCGCTGCTACCGAGTGTGGTACGCGCTGCCAGCGCTGGCTGTGGTGGACCTCATCGTGGACATCATGTTTATT-1458
 E G P P A T E C G Y A C Q P L A V V D L I V D I M F I -464
 GTGGACATCCTCATCAACTTCCGCACCACCTACGTCAATGCCAACGAGGAGGTGGTCAGCCACCCCGCCGATCGCCGTC-1539
 V D I L I N F R T T Y V N A N E E V V S H P G R I A V -491
 CACTACTTCAAGGGCTGGTTCCTCATCGACATGGTGGCCGCCATCCCCTTCGACCTGCTCATCTTCGGCTCTGGCTCTGAG-1620
 H Y F K G W F L I D M V A A I P F D L L I F G S G S E -518
 GAGCTGATCGGGCTGCTGAAGACTGCGCGGCTGCTGCGGCTGGTGGCGTGGCGGGAAGCTGGATCGCTACTCAGAGTAC-1701
 E L I G L L K T A R L L R L V R V A R K L D R Y S E Y -545
 GGCGCGCGCTGCTGTTCTTGTCTCATGTGCACCTTTGCGCTCATCGCGCACTGGCTAGCCTGCATCTGGTACGCCATCGGC-1782
 G A A V L F L L M C T F A L I A H W L A C I W Y A I G -572
 AACATGGAGCAGCCACACATGGACTCACGCATCGGCTGGCTGACCAACCTGGGGCAGCAGATAGGCAAACCTTACAACAGC-1863
 N M E Q P H M D S R I G W L H N L G D Q I G K P Y N S -599
 AGCGGCTGGGCGGCCCTCCATCAAGGACAAGTATGTGACGGCGCTTACTTCACTTACAGCAGCTCACCAGTGTGGGC-1944
 S G L G G P S I K D K Y V T A L Y F T F S S L T S V G -626
 TTCGGCAACGTCTCTCCCAACCAACTCAGAGAAGATCTTCTCCATCTGCGTCATGCTATTGGCTCCCTCATGTATGCT-2025
 F G N V S P N T N S E K I F S I C V M L I G S L M Y A -653

FIG. 8A

AGCATCTTCGGCAACGTGTGCGCCATCATCCAGCGGCTGTACTCGGGCACAGCCGCTACCACACACAGATGCTGCGGGTG-2106
 S I F G N V S A I I O R L Y S G T A R Y H T Q M L R V -680

CGGGAGTTTCATCCGCTTCCACCAGATCCCCAATCCCCTGCGCCAGCGCCTCGAGGAGTACTTCCAGCACGCCTGGTCTTAC-2187
 R E F I R F H Q I P N P L R Q R L E E Y F Q H A W S Y -707

▽

ACCAACGGCATCGACATGAACGCGGTGCTGAAGGGCTTCCCTGAGTGCCTGCAGGCTGACATCTGCCTGCACCTGAACCGC-2268
 T N G I D M N A V L K G F P E C L Q A D I C L H L N R -734
 TCACTGCTGCAGCACTGCAAACCTTCCGAGGGGCCACCAAGGGCTGCCTTCGGGCGCTGGCCATGAAGTTCAAGACCACA-2349
 S L L Q H C K P F R G A T K G C L R A L A M K F K T T -761
 CATGCACCGCCAGGGGACACACTGGTGCATGCTGGGGACCTGCTCACCGCCTGTACTTCATCTCCCGGGGCTCCATCGAG-2430
 H A P P G D T L V H A G D L L T A L Y F I S R G S I E -788

▽

ATCCTGCGGGGCGACGTCGTCGTGGCCATCCTGGGGAAGAATGACATCTTTGGGGAGCCTCTGAACCTGTATGCAAGGCCT-2511
 I L R G D V V V A I L G K N D I F G E P L N L Y A R P -815

cNBD

GGCAAGTCGAACGGGGATGTGCGGGCCCTCACCTACTGTGACCTACACAAGATCCATCGGGACGACCTGCTGGAGGTGCTG-2592
 G K S N G D V R A L T Y C D L H K I H R D D L L E V L -842

▽

GACATGTACCCTGAGTTCTCCGACCACTTCTGGTCCAGCCTGGAGATCACCTTCAACCTGCGAGATACCAACATGATCCCG-2673
 D M Y P E F S D H F W S S L E I T F N L R D T N M I P -869
 GGCTCCCCCGGCAGTACGGAGTTAGAGGGTGGCTTCAGTCGGCAACGCAAGCGCAAGTTGTCTTCCGAGGCGCACGGAC-2754
 G S P G S T E L E G G F S R Q R K R K L S F R R R T D -896

▽

AAGGACACGGAGCAGCCAGGGGAGGTGTGCGCCTTGGGGCCGGGCGGGGCGGGGCGAGGCGGAGTAGCCGGGGCCGGCCG-2835
 K D T E Q P G E V S A L G P G R A G A G P S S R G R P -923
 GGGGGGCGGTGGGGGAGAGCCCGTCCAGTGGCCCCCTCCAGCCCTGAGAGCAGTGAGGATGAGGGCCAGGCCGAGCTCC-2916
 G G P W G E S P S S G P S S P E S S E D E G P G R S S -950
 AGCCCCCTCCGCTGGTGCCTTCTCCAGCCCCAGGCCCGGAGAGCCGCGGGTGGGGAGCCCTGATGGAGGACTGC-2997
 S P L R L V P F S S P R P P G E P P G G E P L M E D C -977

▽

GAGAAGAGCAGCGACACTTGCAACCCCTGTGAGGCGCCTTCTCAGGAGTGTCGAACATTTTCAGCTTCTGGGGGACAGT-3078
 E K S S D T C N P L S G A F S G V S N I F S F W G D S -1004
 CGGGGCGCCAGTACCAGGAGCTCCCTCGATGCCCGCCCCACCCCAAGCCTCCTCAACATCCCCCTCTCCAGCCCGGT-3159
 R G R Q Y Q E L P R C P A P T P S L L N I P L S S P G -1031

▽

CGGCGGCCCCGGGGCGACGTGGAGAGCAGGCTGGATGCCCTCCAGCGCCAGCTCAACAGGCTGGAGACCCGGCTGAGTGCA-3240
 R R P R G D V E S R L D A L Q R Q L N R L E T R L S A -1058
 GACATGGCCACTGTCTGACAGTGTACAGAGGCAGATGACGCTGGTCCGCGCCGCTACAGTGTGTGACCACCCCGGG-3321
 D M A T V L Q L L Q R Q M T L V P P A Y S A V T T P G -1085

▽

CCTGGCCCCACTTCCACATCCCCGCTGTTGCCCGTCAGCCCCCTCCCCACCCTCACCTTGGACTCGCTTCTCAGGTTTCC-3402
 P G P T S T S P L L P V S P L P T L T L D S L S Q V S -1112
 CAGTTTCATGGCGTGTGAGGAGTGGCCCCGGGGCCCCAGAGCTTCCCCAAGAAGGCCCCACACGACGCTCTCCCTACCG-3483
 Q F M A C E E L P P G A P E L P Q E G P T R R L S L P -1139
 GGCCAGCTGGGGCCCTCACCTCCCAGCCCCGTCACAGACACGGCTCGGACCCGGGCAGTTAGTGGGGCTGCCAGTGTGG-3564
 G Q L G A L T S Q P L H R H G S D P G S * -1159
 ACACGTGGCTCACCCAGGGATCAAGGCGCTGCTGGGCGCTCCCCTTGGAGGCCCTGCTCAGGAGGCCCTGACCGTGGAG-3645
 GGGAGAGGAACTCGAAAGCACAGCTCCTCCCCAGCCCTTGGGACCATCTTCTCCTGCAGTCCCCTGGGCCCCAGTGAG-3726
 GGGCAGGGGCGAGGCGGCGAGTAGGTGGGCGCTGTGGTCCCCCATGCTGAGGGCATTAGCTGGTCTAACTGCCCGGA-3807
 GGCACCCGCGCTGGGCCTTAGGCACCTCAAGGACTTTTCTGCTATTCTATTGTTAAGGATAATAATTAAGGA-3888
 TCATATGAATAATTAATGAAGATGCTGATGACTATGAATAATAATAATTATCCTGAGGAG (A) n -3949

FIG. 8B

K2287

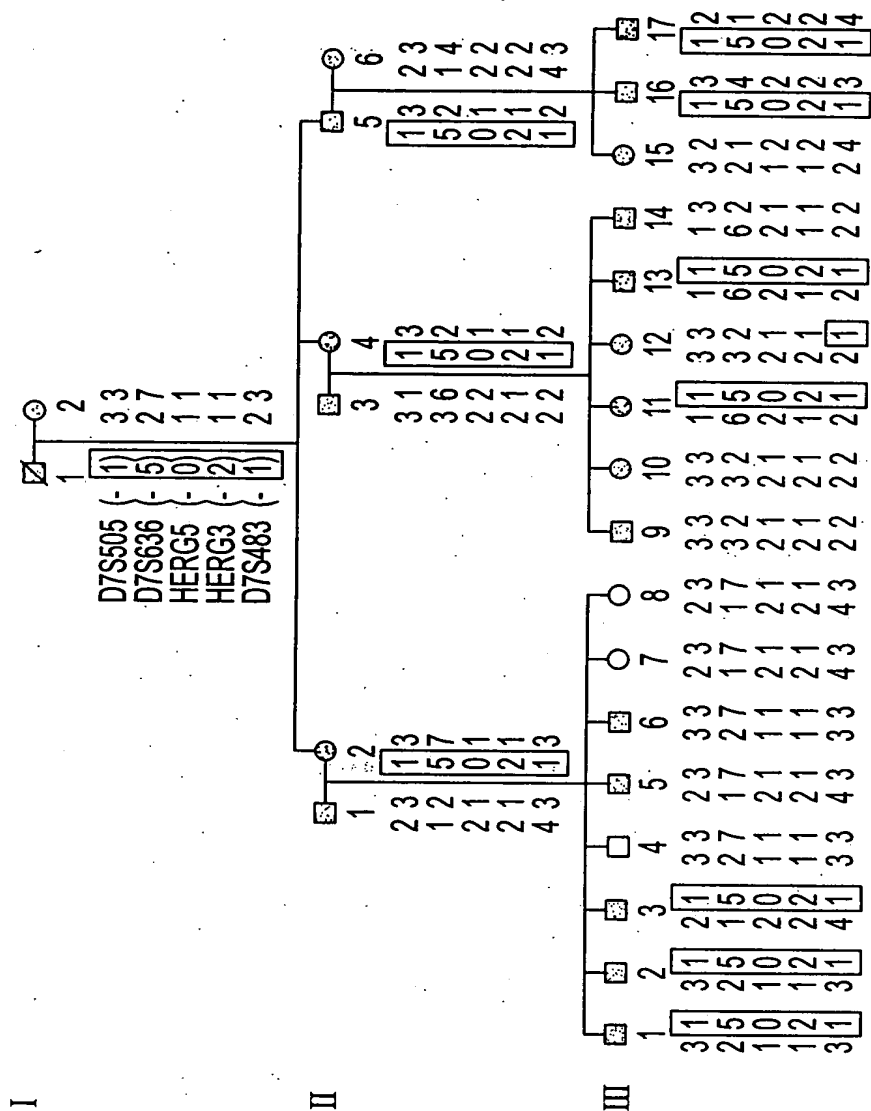


FIG. 9B

K1956

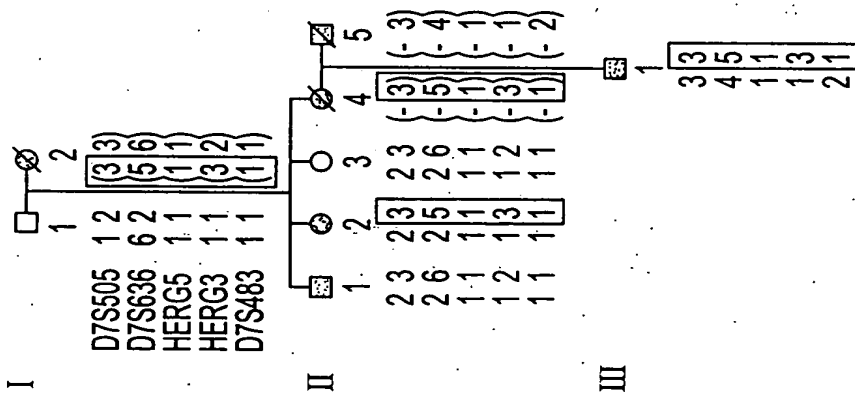


FIG. 9A

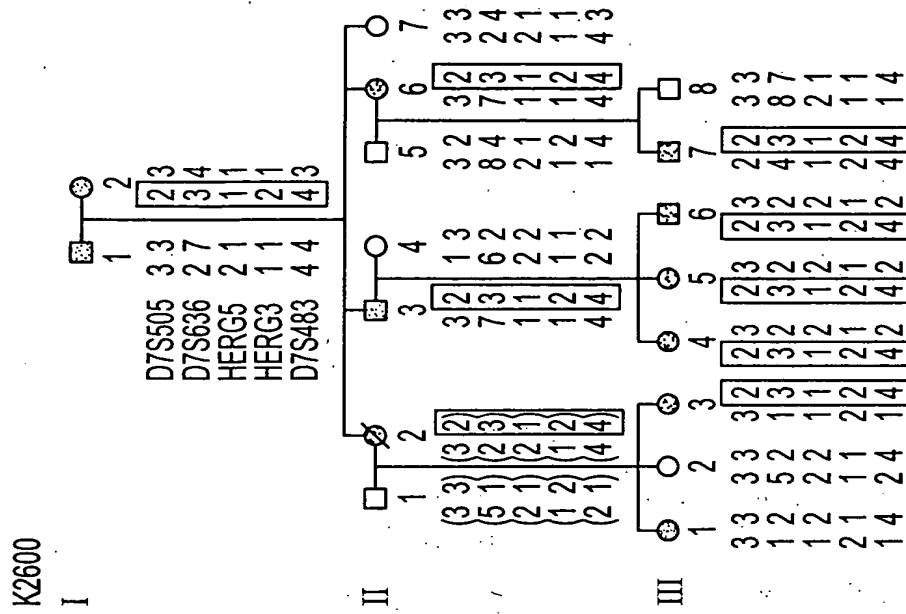


FIG. 9D

FIG. 9E

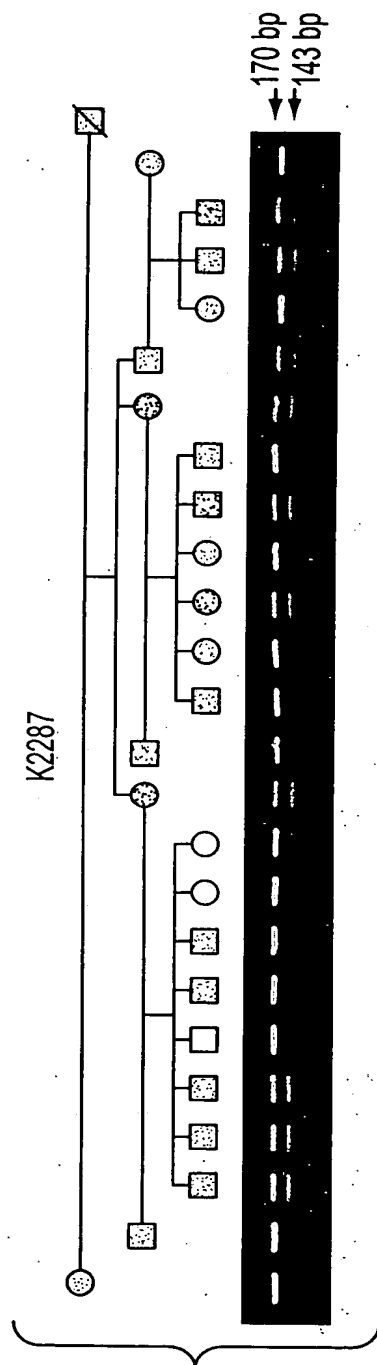


FIG. 10A

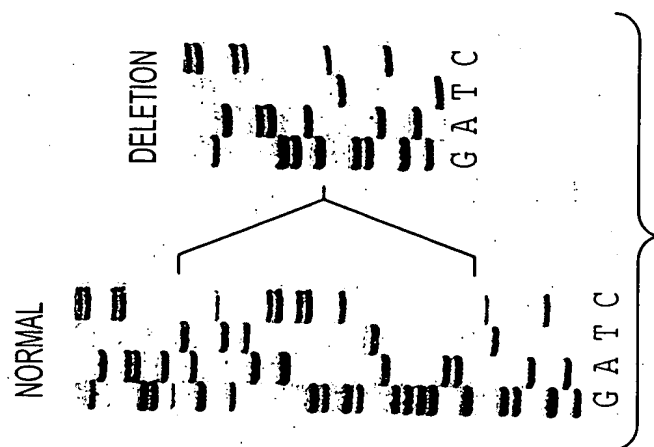


FIG. 10B

TGG TTC CTC ATC GAC ATG GTG GCC GCC ATC CCC TTC GAC CTG CTC SEQ ID NO:96
 W F L I D M V A A I P F D L L SEQ ID NO:97
 S3

FIG. 10C

NORMAL GTC ATC TAC ACG GCT GTC TTC ACA CCC TAC TCG GCT GCC TTC CTG CTG AAG GAG SEQ ID NO:98
 V I Y T A V F T P Y S A A F L L K E SEQ ID NO:99

DELETION GTC ATC TAC CGG CTG TCT TCA CAC CCT ACT CGG CTG CCT TCC TGC TGA SEQ ID NO:100
 V I Y R L S S H P T R L P S C SEQ ID NO:101

FIG. 11C

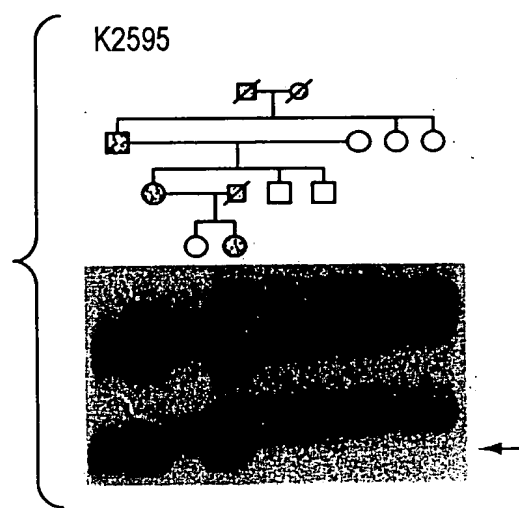


FIG. 11A

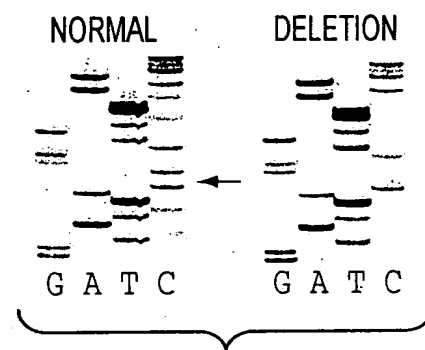


FIG. 11B

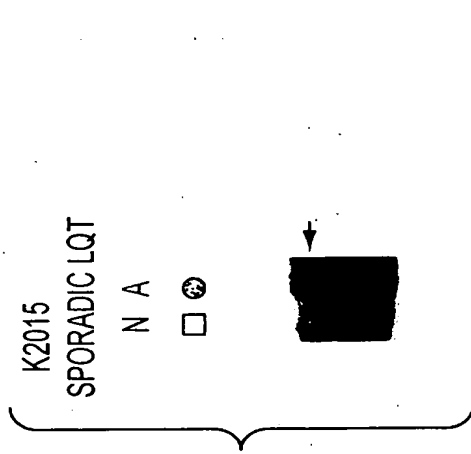


FIG. 12E

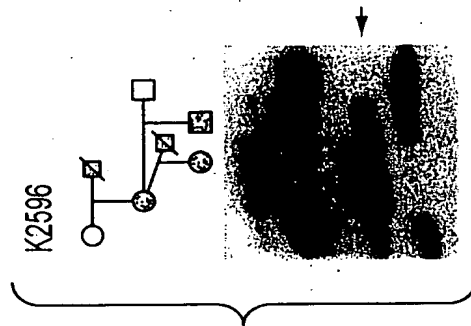


FIG. 12C

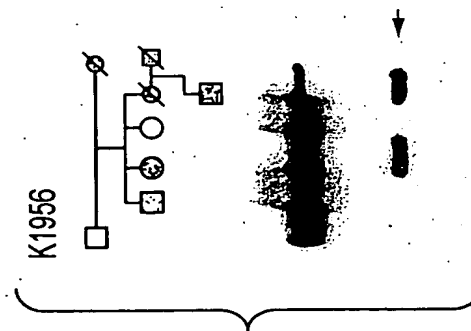


FIG. 12A

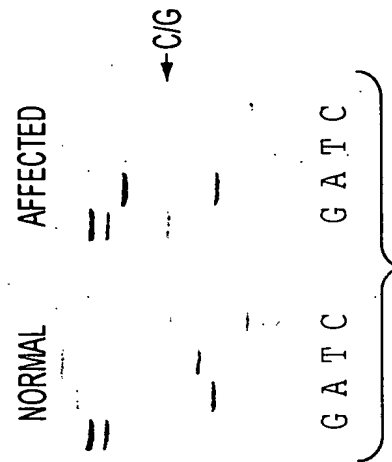


FIG. 12F

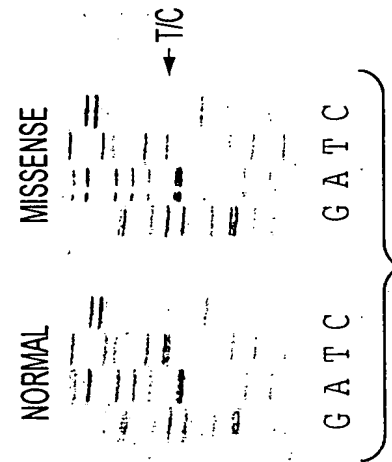


FIG. 12D

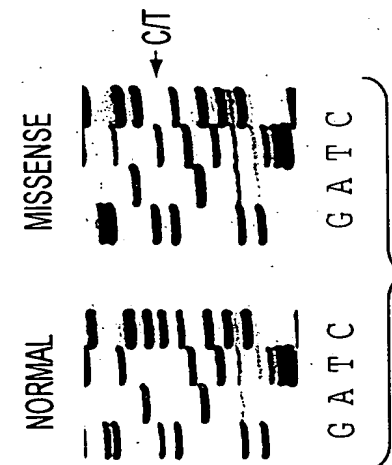


FIG. 12B

	GTG → V	SEQ ID
	GCG	NO:
	\\	
	L I A H W L	102
	↔ S5 ↔	
K1956	L I V H W L	103
H-Erg	L I A H W L	102
M-Eag	L A A H W K	104
R-Eag	L A A H W M	105
Eag	L V A H W L	106
Elk	L A A H W L	107

	GAC → D	SEQ ID
	AAC	NO:
	\\	
	D I L I N F R	108
	↔ S2 ↔	
K2596	D I L I D F R	109
H-Erg	D I L I N F R	108
M-Eag	D I V L N F H	110
R-Eag	D I V L N F H	110
Eag	D I V L N F H	110
Elk	D I L L N F R	111

FIG. 12G

5'-CAT CCT GG // gtagggg-3'
 ↓
 C

FIG. 12I

FIG. 12H

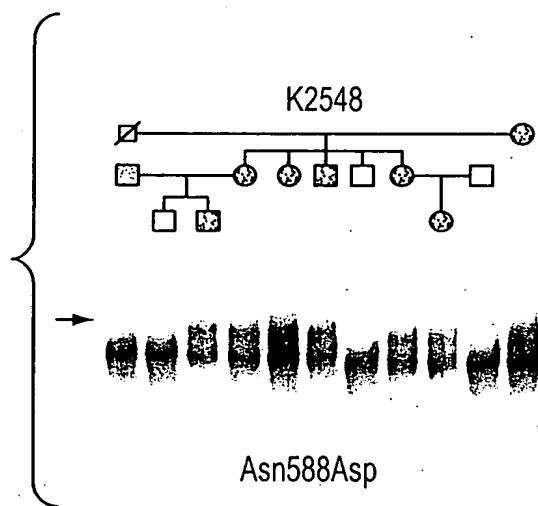


FIG. 13A

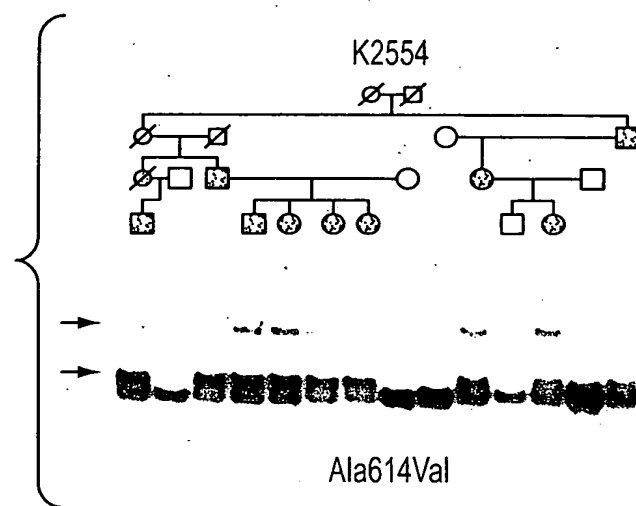


FIG. 13B

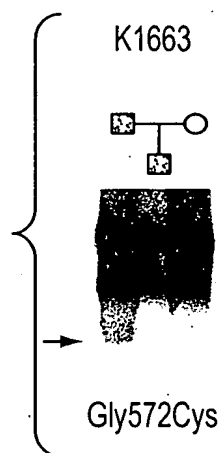


FIG. 13C

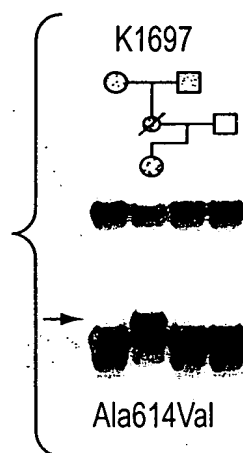


FIG. 13D

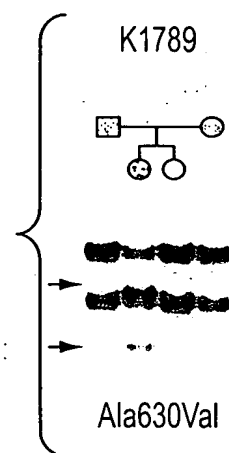


FIG. 13E

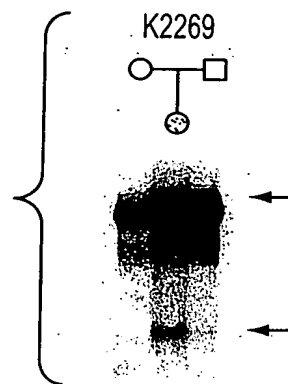


FIG. 14A

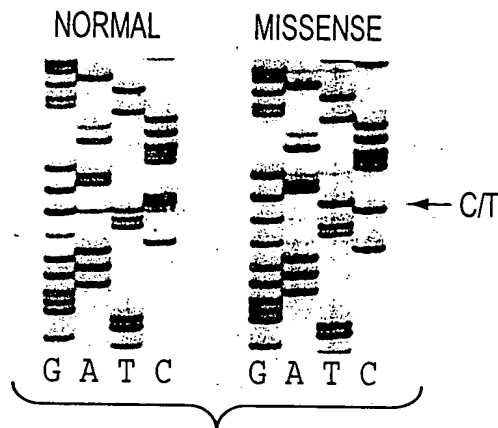


FIG. 14B

	AGC → S	SEQ ID
	GGC	NO:
	SVGFGNVS	112
	← PORE →	
K2269	SVGFSNVS	113
H-Erg	SVGFGNVS	112
M-Eag	SVGFGNIA	114
R-Eag	SVGFGNIA	114
Eag	SVGFGNVA	115
Elk	SVGFGNVS	112
Shaker	TVGYGDMT	116

FIG. 14C

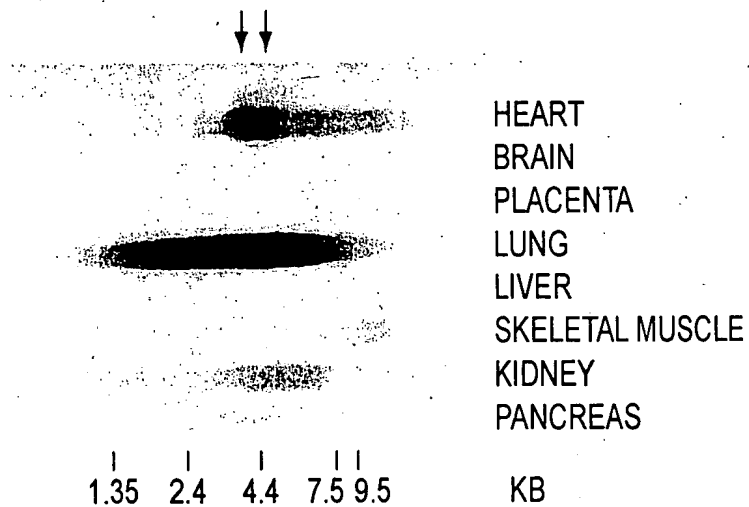


FIG. 15